Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 21:58:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716166.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR9716166 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716166.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 21:58:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716166.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,349,833
Mapped reads	2,092,569 / 89.05%
Unmapped reads	257,264 / 10.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,612 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	84,515 / 3.6%
Duplication rate	3.12%
Clipped reads	2,099,210 / 89.33%

2.2. ACGT Content

Number/percentage of A's	30,980,842 / 26.14%
Number/percentage of C's	22,496,387 / 18.98%
Number/percentage of T's	37,230,285 / 31.42%
Number/percentage of G's	27,796,263 / 23.46%
Number/percentage of N's	1,709 / 0%
GC Percentage	42.44%

2.3. Coverage

Mean	0.0383

Standard Deviation	0.3129

2.4. Mapping Quality

Mean Mapping Quality	43.28

2.5. Mismatches and indels

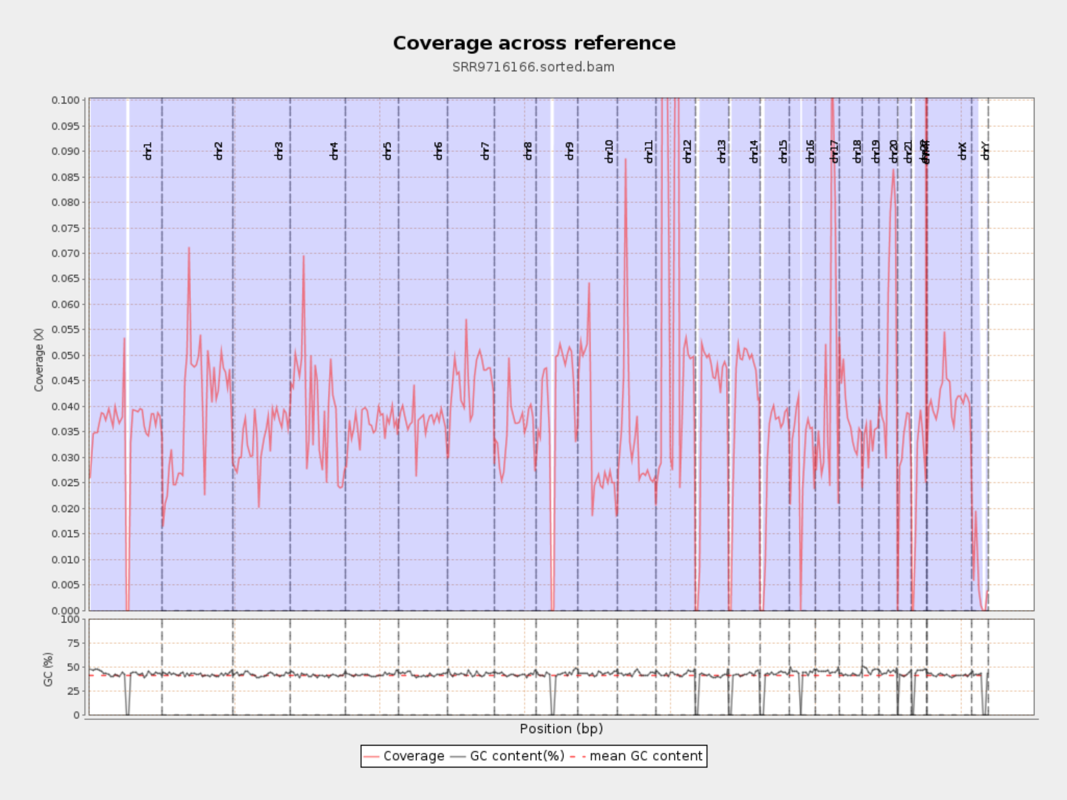
General error rate	0.55%
Mismatches	638,300
Insertions	8,358
Mapped reads with at least one insertion	0.4%
Deletions	18,643
Mapped reads with at least one deletion	0.88%
Homopolymer indels	39.9%

2.6. Chromosome stats

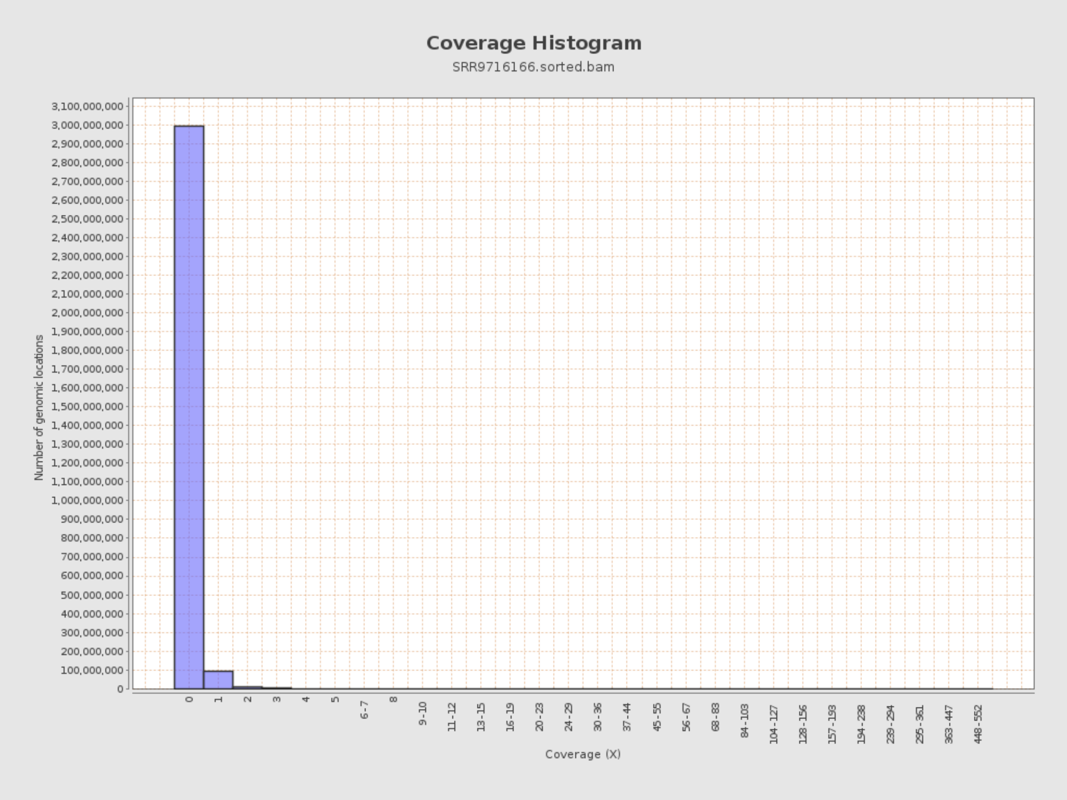
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8771715	0.0352	0.4752
chr2	243199373	9703189	0.0399	0.3667
chr3	198022430	6722278	0.0339	0.2028
chr4	191154276	7516428	0.0393	0.2507
chr5	180915260	6596898	0.0365	0.2127
chr6	171115067	6360933	0.0372	0.2374
chr7	159138663	7199812	0.0452	0.3489

chr8	146364022	5201457	0.0355	0.298
chr9	141213431	5682246	0.0402	0.3585
chr10	135534747	4619050	0.0341	0.347
chr11	135006516	4708951	0.0349	0.2808
chr12	133851895	9043204	0.0676	0.3247
chr13	115169878	4595066	0.0399	0.2184
chr14	107349540	4386709	0.0409	0.2652
chr15	102531392	3053315	0.0298	0.1897
chr16	90354753	2776563	0.0307	0.2204
chr17	81195210	3624409	0.0446	0.2414
chr18	78077248	2993202	0.0383	0.6049
chr19	59128983	1998633	0.0338	0.3653
chr20	63025520	3556470	0.0564	0.2746
chr21	48129895	1454454	0.0302	0.2275
chr22	51304566	1205607	0.0235	0.1674
chrMT	16571	14417	0.87	1.1686
chrX	155270560	6415652	0.0413	0.2774
chrY	59373566	336044	0.0057	0.1409

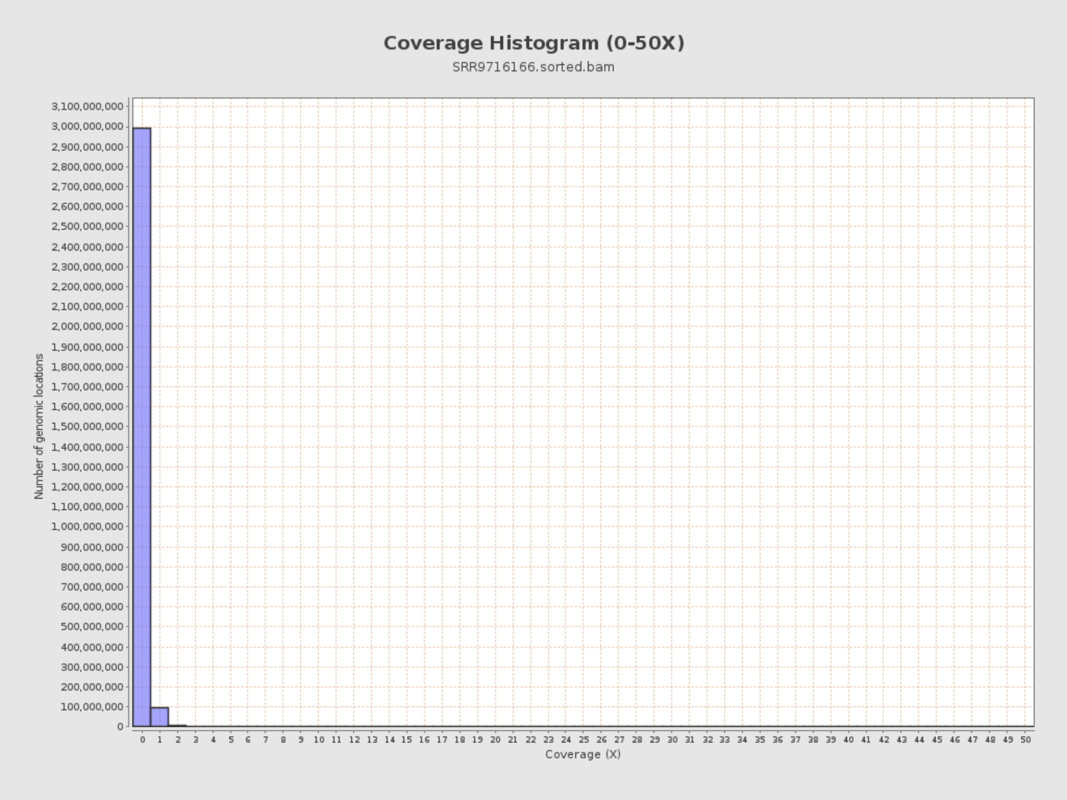
3. Results : Coverage across reference



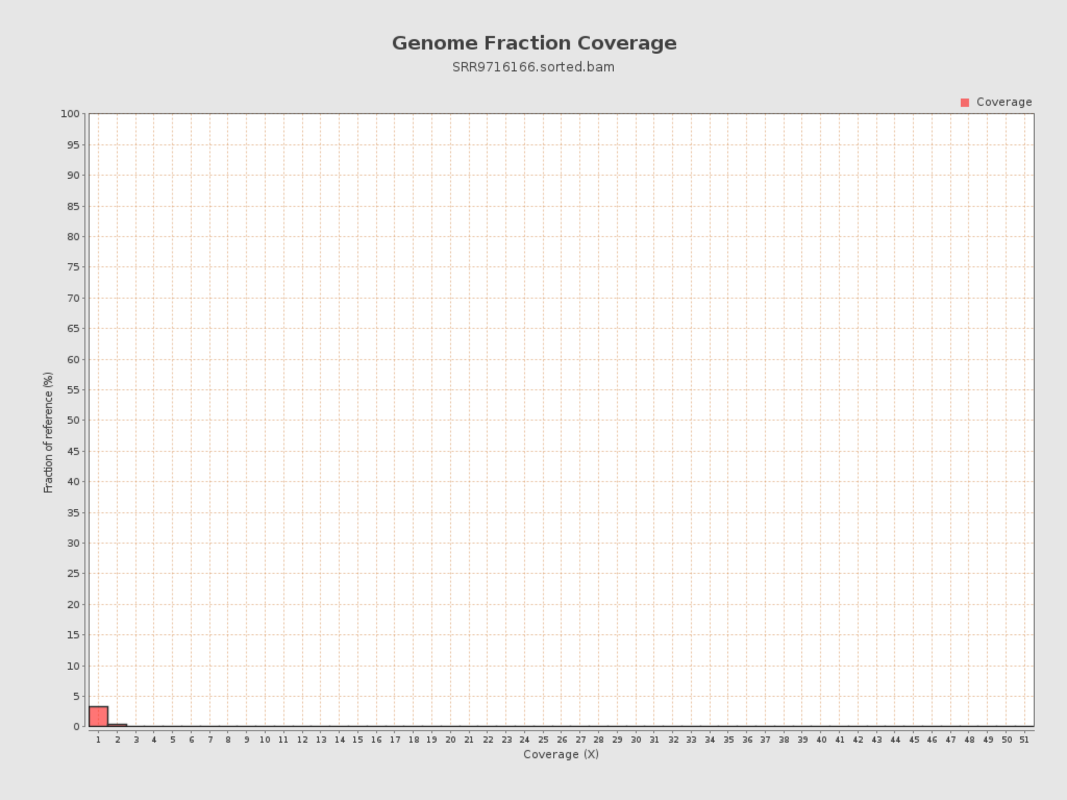
4. Results : Coverage Histogram



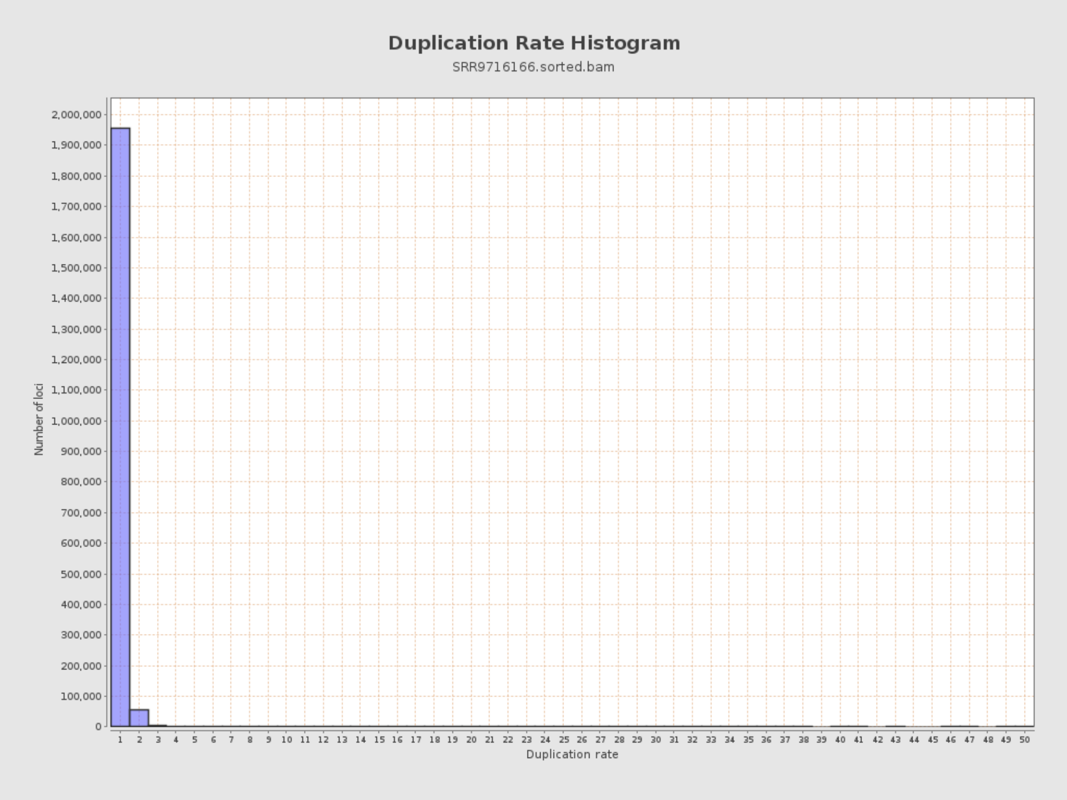
5. Results : Coverage Histogram (0-50X)



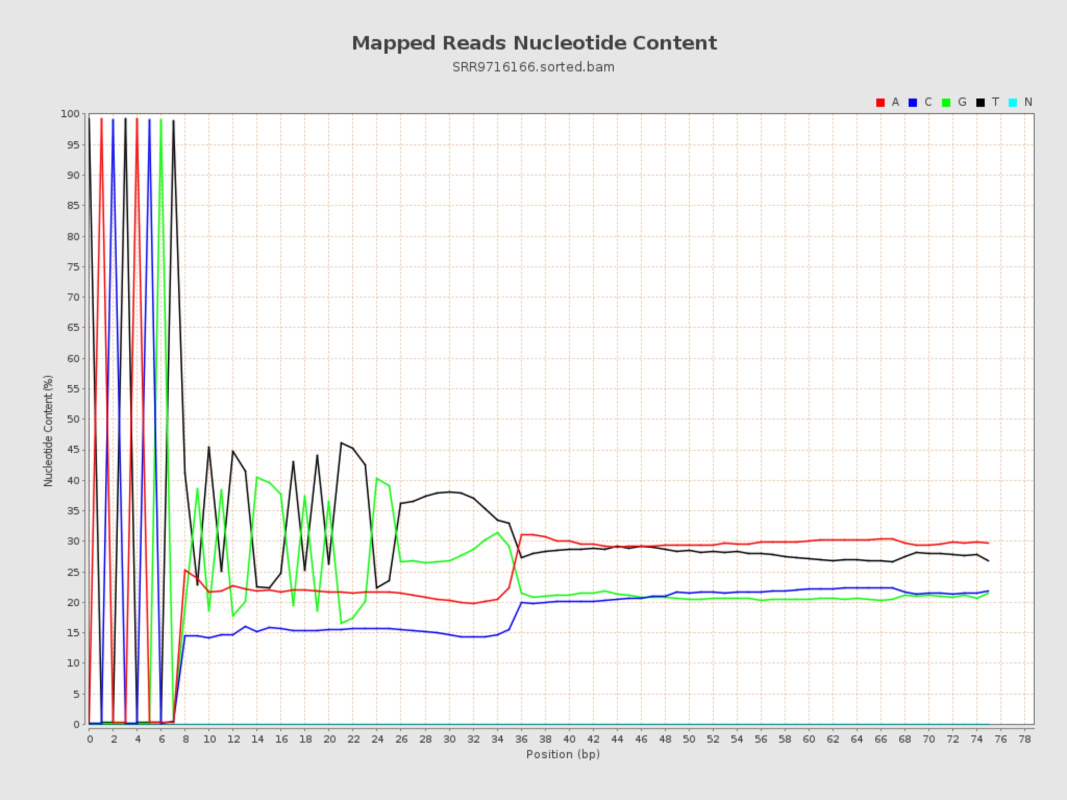
6. Results : Genome Fraction Coverage



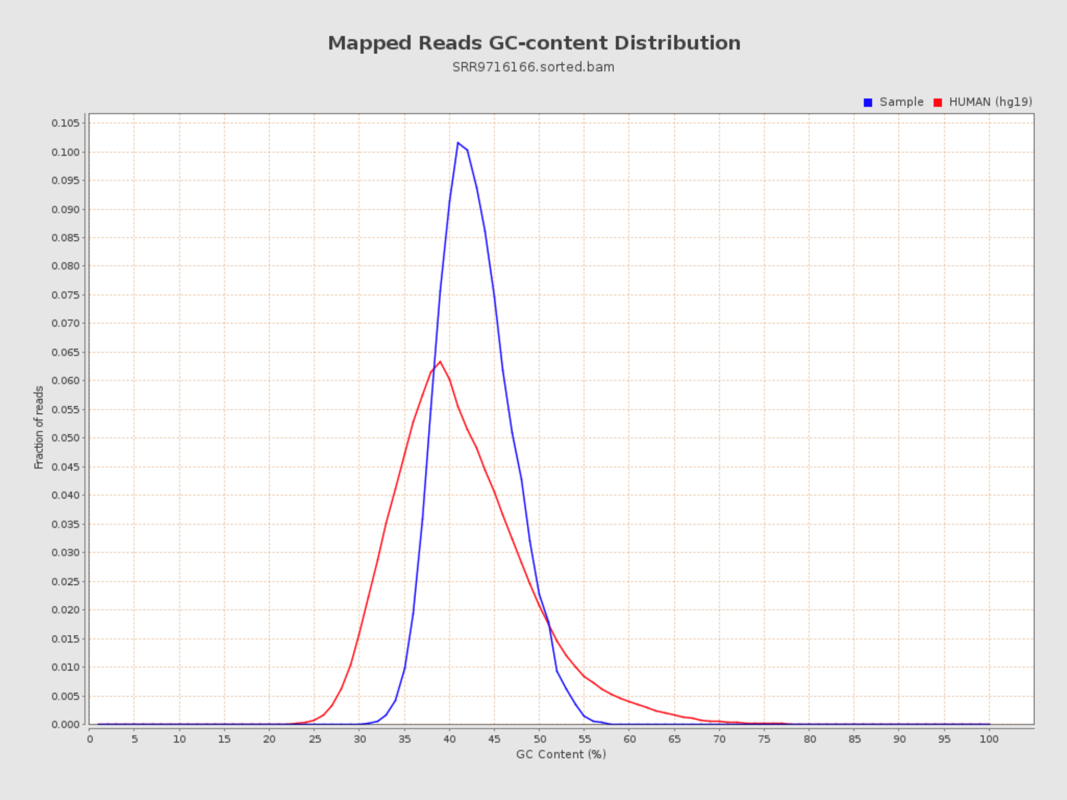
7. Results : Duplication Rate Histogram



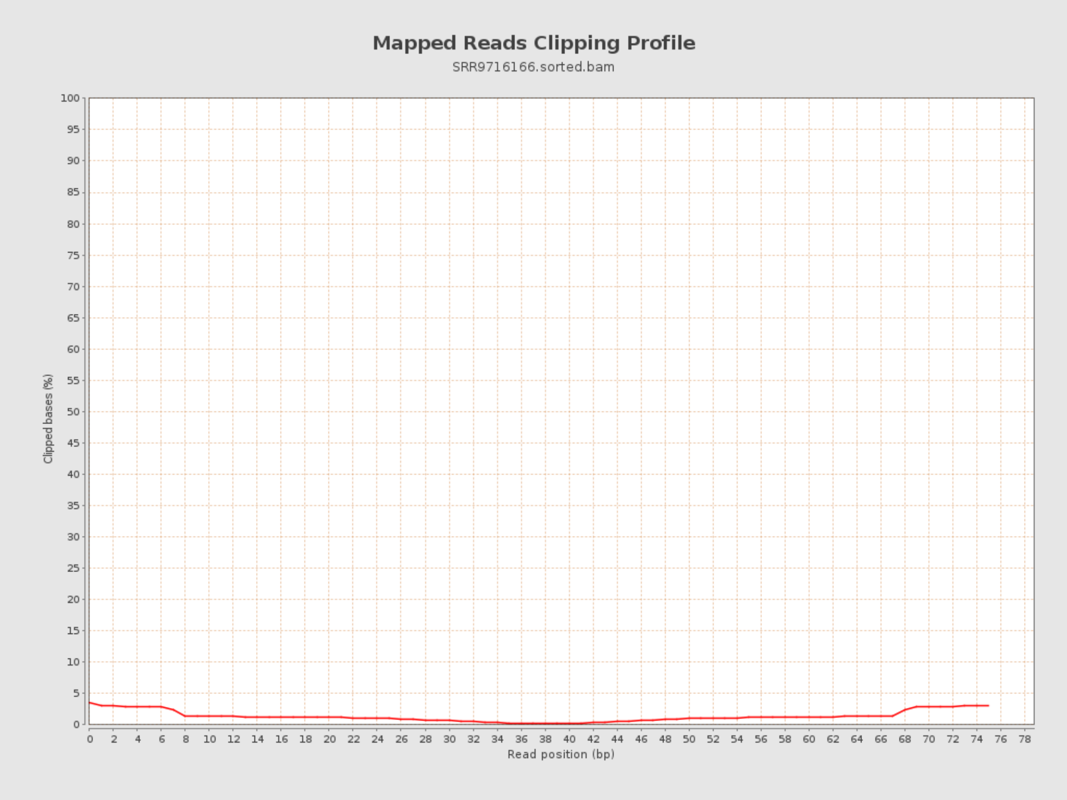
8. Results : Mapped Reads Nucleotide Content



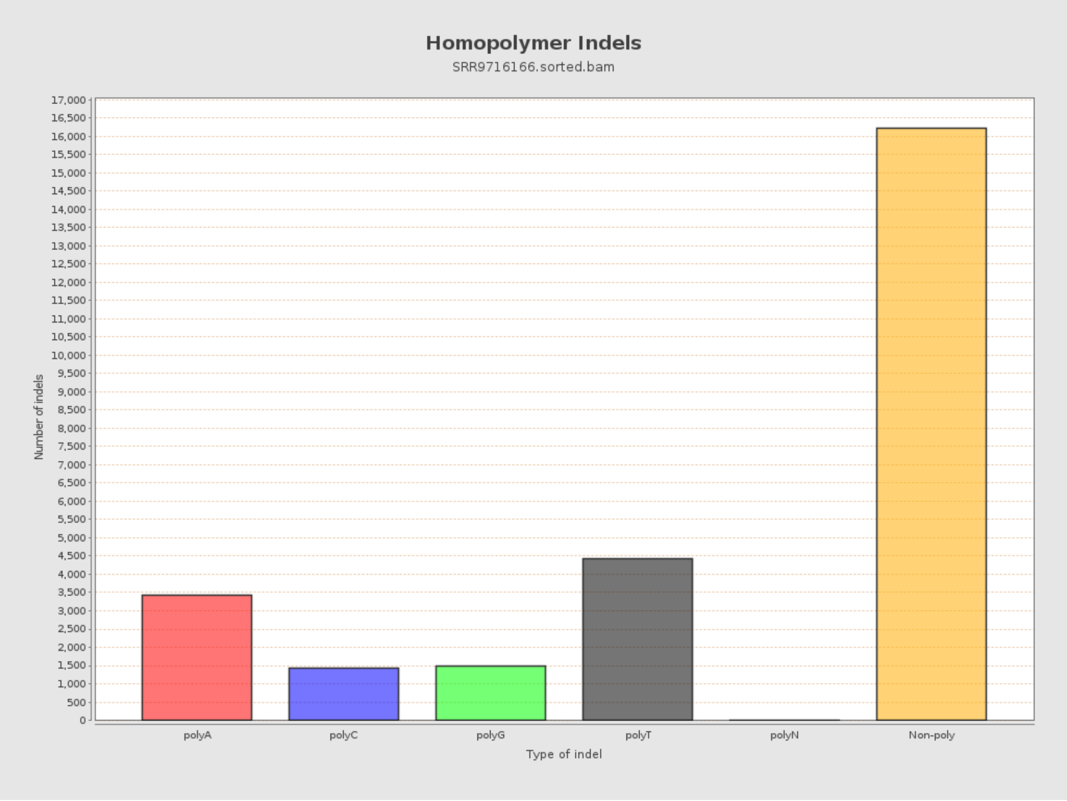
9. Results : Mapped Reads GC-content Distribution



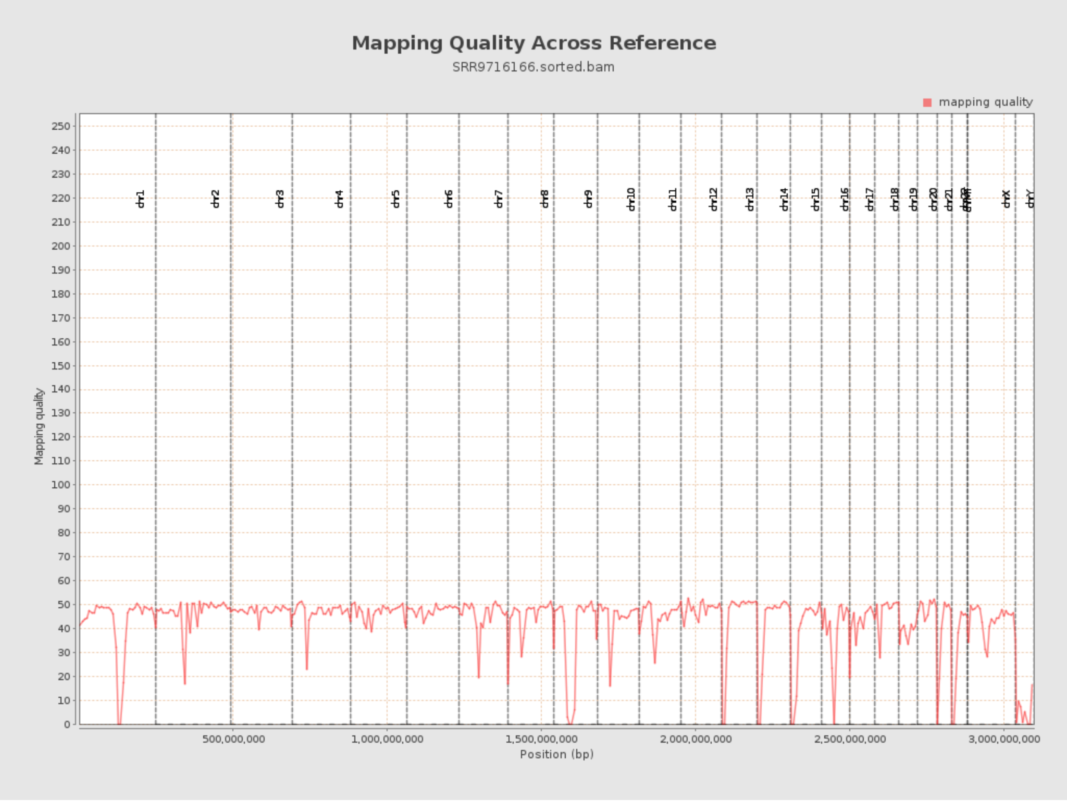
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram